Please replace the paragraph beginning at page 4, line 3, with the following rewritten paragraph:

--FIG. 2 shows the 361 amino acid sequence that is coded for by gene O1-180 (SEQ ID NO: 2).--

Please replace the paragraph beginning at page 4, line 4, with the following rewritten paragraph:

--FIG. 3 shows the 1817 base pair cDNA sequence of gene O1-184 (SEQ ID NO: 3).--

Please replace the paragraph beginning at page 4, line 5, with the following rewritten paragraph:

--FIG. 4 shows the 426 amino acid sequence that is coded for by gene O1-184 (SEQ ID NO: 4).--

Please replace the paragraph beginning at page 4, line 6, with the following rewritten paragraph:

--FIG. 5 shows the 1019 base pair cDNA sequence of gene O1-236 (SEQ ID NO: 5).--

Please replace the paragraph beginning at page 4, line 7, with the following rewritten paragraph:

--FIG. 6 shows the 207 amino acid sequence that is coded for by gene O1-236 (SEQ ID NO: 6)--

Please replace the paragraph beginning at page 4, line 30, with the following rewritten paragraph:

--FIG. 10. Npm2 cDNA representation. Schematic representation of the mouse Npm2 cDNA sequence (984 bp) and two of the clones isolated from the mouse ovary CDNA libraries. The original 01-236 probe (749 bp) is shown at the top and encompasses the entire Npm2 open reading frame. The open reading frame (solid box) is 621 bp and the 5' UTR and 3' UTR sequences (thin lines) are 155 bp and 205 bp, respectively. The polyA sequences are not depicted. Clone 236-1 was isolated from the wild-type ovary cDNA library and clone 236-3 was isolated from the GDF-9-deficient ovary cDNA library. Clone 236-3 (984 bp excluding polyA sequence) is 4 bp longer at the 5' end and 1 bp longer at the 3' end than clone 236-1 (979 bp

excluding polyA sequences). Codon 36 of the open reading frame of both cDNAs is GGC (Glycine; Figure 11) whereas the same codon of the 129SvEv gene is TGC (Cysteine; Figures 13A and 13B (SEQ ID NO: 7 through SEQ ID NO: 14)).--

Please replace the paragraph beginning at page 5, line 28, with the following rewritten paragraph:

--FIGS. 13A and 13B. Mouse Npm2 gene (SEQ ID NO: 7 through SEQ ID NO: 14) and amino acid sequences. Uppercase letters represent sequence identity with the Npm2 cDNA sequences; non-transcribed 5' and 3' sequences and intron sequences are shown in lowercase. The predicted transcription initiation codon, the termination codon, and the polyadenylation signal sequence are all underlined. Numbers along the left side represent the amino acids. The underlined and bolded "T" in codon 36, the bolded "c" for amino acid 26, and the underlined and bolded "C: in the 3' UTR sequence indicate differences between the cDNA and gene sequences. Arrows indicate where the O1-236 fragment initiates and ends in the cDNA sequence.--

Please replace the paragraph beginning at page 10, line 15, with the following rewritten paragraph:

--Fragments of proteins are seen to include any peptide that contains 6 contiguous amino acids or more that are identical to 6 contiguous amino acids of either of the sequences shown in Figures 2 (SEQ ID NO: 2), 4 (SEQ ID NO: 4), 6 (SEQ ID NO: 6), 11 and 14. Fragments that contain 7, 8, 9, 10, 11, 12, 13, 14 and 15 or more contiguous amino acids or more that are identical to a corresponding number of amino acids of any of the sequences shown in Figures 2 (SEQ ID NO: 2), 4 (SEQ ID NO: 4), 6 (SEQ ID NO: 6), 11 and 14 are also contemplated. Fragments may be used to generate antibodies. Particularly useful fragments will be those that make up domains of O1-180, O1-184 or O1-236. Domains are defined as portions of the proteins having a discrete tertiary structure and that is maintained in the absence of the remainder of the protein. Such structures can be found by techniques known to those skilled in the art. The protein is partially digested with a protease such as subtilisin, trypsin, chymotrypsin or the like and then subjected to polyacrylamide gel electrophoresis to separate the protein fragments. The fragments can then

be transferred to a PVDF membrane and subjected to micro sequencing to determine the amino acid sequence of the N-terminal of the fragments.--

Please replace the paragraph beginning at page 29, line 5, with the following rewritten paragraph:

--One of the full length Npm2 cDNAs (clone 236-1) was used to screen a mouse 129SvEv genomic library (Stratagene) to identify the mouse Npm2 gene. 500,000 phage were screened and 12 positive were identified. Two of these overlapping phage clones, 236-13 and 236-14 (~37 kb of total genomic sequence), were used to determine the structure of the mouse Npm2 gene. The mouse Npm2 is encoded by 9 exons and spans ~6.6 kb (Figures 12 and 13A and 13B (SEQ ID NO: 7-14)). Two moderate size introns (introns 4 and 5) contribute the majority of the gene size. The initiation ATG codon resides in exon 2 and the termination codon in exon 9. The splice donor and acceptor sites (Figures 13A and 13B (SEQ ID NO: 7-14)) match well with the consensus sequences found in rodents, and all of the intron-exon boundaries conform to the "GT-AG" rule (Senapathy et al. Methods Enzymol 183:252-278 (1990)). A consensus polyadenylation signal sequence (AATAAA) is found upstream of the polyA tracts which are present in the two isolated cDNAs (Figures 13A and 13B (SEQ ID NO: 7-14)).--

In the claims:

Please amend claim 1 as follows:

1. (Amended) Substantially pure O1-180 having the amino acid sequence set forth in Fig. 2 (SEQ ID NO: 2).

Please amend claim 2 as follows:

2. (Amended) An isolated polynucleotide having the polynucleotide sequence set forth in Fig. 1 (SEQ ID NO: 1).